

0590
0530 # 10

OIIPE

RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/09/812,238B

TIME: 15:13:29

Input Set : A:\GZ 2094.00 Sequence Listing.txt

Output Set: N:\CRF3\06062002\I812238B.raw

3 <110> APPLICANT: Nicolette, Charles
 5 <120> TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
 8 <130> FILE REFERENCE: GZ 2094.00
 10 <140> CURRENT APPLICATION NUMBER: 09/812,238B
 C--> 11 <141> CURRENT FILING DATE: 2002-05-21
 13 <160> NUMBER OF SEQ ID NOS: 19
 15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2130
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (22)...(2004)
 26 <400> SEQUENCE: 1
 27 cgcggaatcc ggaagaacac a atg gat ctg gtg cta aaa aga tgc ctt ctt 51
 28 Met Asp Leu Val Leu Lys Arg Cys Leu Leu
 29 1 5 10
 31 cat ttg gct gtg ata ggt gct ttg ctg gct gtg ggg gct aca aaa gta 99
 32 His Leu Ala Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr Lys Val
 33 15 20 25
 35 ccc aga aac cag gac tgg ctt ggt gtc tca agg caa ctc aga acc aaa 147
 36 Pro Arg Asn Gln Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Thr Lys
 37 30 35 40
 39 gcc tgg aac agg cag ctg tat cca gag tgg aca gaa gcc cag aga ctt 195
 40 Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu
 41 45 50 55
 43 gac tgc tgg aga ggt ggt caa gtg tcc ctc aag gtc agt aat gat ggg 243
 44 Asp Cys Trp Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn Asp Gly
 45 60 65 70
 47 cct aca ctg att ggt gca aat gcc tcc ttc tct att gcc ttg aac ttc 291
 48 Pro Thr Leu Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe
 49 75 80 85 90
 51 cct gga agc caa aag gta ttg cca gat ggg cag gtt atc tgg gtc aac 339
 52 Pro Gly Ser Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Val Asn
 53 95 100 105
 55 aat acc atc atc aat ggg agc cag gtg tgg gga gga cag cca gtg tat 387
 56 Asn Thr Ile Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro Val Tyr
 57 110 115 120
 59 ccc cag gaa act gac gat gcc tgc atc ttc cct gat ggt gga cct tgc 435
 60 Pro Gln Glu Thr Asp Asp Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys
 61 125 130 135
 63 cca tct ggc tct tgg tct cag aag aga agc ttt gtt tat gtc tgg aag 483

ENTERED

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64	Pro	Ser	Gly	Ser	Trp	Ser	Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	
65		140					145					150					
67	acc	tgg	ggc	caa	tac	tgg	caa	gtt	cta	ggg	ggc	cca	gtg	tct	ggg	ctg	531
68	Thr	Trp	Gly	Gln	Tyr	Trp	Gln	Val	Leu	Gly	Gly	Pro	Val	Ser	Gly	Leu	
69	155					160				165					170		
71	agc	att	ggg	aca	ggc	agg	gca	atg	ctg	ggc	aca	cac	acc	atg	gaa	gtg	579
72	Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly	Thr	His	Thr	Met	Glu	Val	
73					175					180					185		
75	act	gtc	tac	cat	cgc	cgg	gga	tcc	cgg	agc	tat	gtg	cct	ctt	gct	cat	627
76	Thr	Val	Tyr	His	Arg	Arg	Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	
77				190					195					200			
79	tcc	agc	tca	gcc	ttc	acc	att	act	gac	cag	gtg	cct	ttc	tcc	gtg	agc	675
80	Ser	Ser	Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser	Val	Ser	
81		205						210				215					
83	gtg	tcc	cag	ttg	cgg	gcc	ttg	gat	gga	ggg	aac	aag	cac	ttc	ctg	aga	723
84	Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly	Asn	Lys	His	Phe	Leu	Arg	
85		220				225					230						
87	aat	cag	cct	ctg	acc	ttt	gcc	ctc	cag	ctc	cat	gac	ccc	agt	ggc	tat	771
88	Asn	Gln	Pro	Leu	Thr	Phe	Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	
89	235				240				245						250		
91	ctg	gct	gaa	gct	gac	ctc	tcc	tac	acc	tgg	gac	ttt	gga	gac	agt	agt	819
92	Leu	Ala	Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp	Ser	Ser	
93				255					260					265			
95	gga	acc	ctg	atc	tct	cgg	gca	ctt	gtg	gtc	act	cat	act	tac	ctg	gag	867
96	Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val	Thr	His	Thr	Tyr	Leu	Glu	
97				270					275					280			
99	cct	ggc	cca	gtc	act	gcc	cag	gtg	gtc	ctg	cag	gct	gcc	att	cct	ctc	915
100	Pro	Gly	Pro	Val	Thr	Ala	Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	
101		285					290					295					
103	acc	tcc	tgt	ggc	tcc	tcc	cca	gtt	cca	ggc	acc	aca	gat	ggg	cac	agg	963
104	Thr	Ser	Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly	His	Arg	
105	300					305					310						
107	cca	act	gca	gag	gcc	cct	aac	acc	aca	gct	ggc	caa	gtg	cct	act	aca	1011
108	Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	
109	315				320						325				330		
111	gaa	gtt	gtg	ggt	act	aca	cct	ggt	cag	gcg	cca	act	gca	gag	ccc	tct	1059
112	Glu	Val	Val	Gly	Thr	Thr	Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	
113				335					340					345			
115	gga	acc	aca	tct	gtg	cag	gtg	cca	acc	act	gaa	gtc	ata	agc	act	gca	1107
116	Gly	Thr	Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser	Thr	Ala	
117				350					355					360			
119	cct	gtg	cag	atg	cca	act	gca	gag	agc	aca	ggt	atg	aca	cct	gag	aag	1155
120	Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr	Gly	Met	Thr	Pro	Glu	Lys	
121				365				370						375			
123	gtg	cca	gtt	tca	gag	gtc	atg	ggt	acc	aca	ctg	gca	gag	atg	tca	act	1203
124	Val	Pro	Val	Ser	Glu	Val	Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	
125		380				385						390					
127	cca	gag	gct	aca	ggt	atg	aca	cct	gca	gag	gta	tca	att	gtg	gtg	ctt	1251
128	Pro	Glu	Ala	Thr	Gly	Met	Thr	Pro	Ala	Glu	Val	Ser	Ile	Val	Val	Leu	

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129	395		400		405		410	
131	tct gga acc aca gct gca cag gta aca act aca gag tgg gtg gag acc	1299						
132	Ser Gly Thr Thr Ala Ala Gln Val Thr Thr Thr Glu Trp Val Glu Thr							
133		415		420		425		
135	aca gct aga gag cta cct atc cct gag cct gaa ggt cca gat gcc agc	1347						
136	Thr Ala Arg Glu Leu Pro Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser							
137		430		435		440		
139	tca atc atg tct acg gaa agt att aca ggt tcc ctg ggc ccc ctg ctg	1395						
140	Ser Ile Met Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu							
141		445		450		455		
143	gat ggt aca gcc acc tta agg ctg gtg aag aga caa gtc ccc ctg gat	1443						
144	Asp Gly Thr Ala Thr Leu Arg Leu Val Lys Arg Gln Val Pro Leu Asp							
145		460		465		470		
147	tgt gtt ctg tat cga tat ggt tcc ttt tcc gtc acc ctg gac att gtc	1491						
148	Cys Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val Thr Leu Asp Ile Val							
149		475		480		485		
151	cag ggt att gaa agt gcc gag atc ctg cag gct gtg ccg tcc ggt gag	1539						
152	Gln Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser Gly Glu							
153		495		500		505		
155	ggg gat gca ttt gag ctg act gtg tcc tgc caa ggc ggg ctg ccc aag	1587						
156	Gly Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys							
157		510		515		520		
159	gaa gcc tgc atg gag atc tca tcg cca ggg tgc cag ccc cct gcc cag	1635						
160	Glu Ala Cys Met Glu Ile Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln							
161		525		530		535		
163	cgg ctg tgc cag cct gtg cta ccc agc cca gcc tgc cag ctg gtt ctg	1683						
164	Arg Leu Cys Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu Val Leu							
165		540		545		550		
167	cac cag ata ctg aag ggt ggc tcg ggg aca tac tgc ctc aat gtg tct	1731						
168	His Gln Ile Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser							
169		555		560		565		
171	ctg gct gat acc aac agc ctg gca gtg gtc agc acc cag ctt atc atg	1779						
172	Leu Ala Asp Thr Asn Ser Leu Ala Val Val Ser Thr Gln Leu Ile Met							
173		575		580		585		
175	cct ggt caa gaa gca ggc ctt ggg cag gtt ccg ctg atc gtg ggc atc	1827						
176	Pro Gly Gln Glu Ala Gly Leu Gly Gln Val Pro Leu Ile Val Gly Ile							
177		590		595		600		
179	ttg ctg gtg ttg atg gct gtg gtc ctt gca tct ctg ata tat agg cgc	1875						
180	Leu Leu Val Leu Met Ala Val Val Leu Ala Ser Leu Ile Tyr Arg Arg							
181		605		610		615		
183	aga ctt atg aag caa gac ttc tcc gta ccc cag ttg cca cat agc agc	1923						
184	Arg Leu Met Lys Gln Asp Phe Ser Val Pro Gln Leu Pro His Ser Ser							
185		620		625		630		
187	agt cac tgg ctg cgt cta ccc cgc atc ttc tgc tct tgt ccc att ggt	1971						
188	Ser His Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly							
189		635		640		645		
191	gag aat agc ccc ctc ctc agt ggg cag cag gtc tgagtactct catatgatgc	2024						
192	Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln Val							
193		655		660				

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195  tgtgattttc ctggagttga cagaaacacc tatatttccc ccagtcttcc ctgggagact      2084
196  actattaact gaaataaata ctacagagcct gaaaaaaaaa aaaaaa      2130
198  <210> SEQ ID NO: 2
199  <211> LENGTH: 661
200  <212> TYPE: PRT
201  <213> ORGANISM: Homo sapiens
203  <400> SEQUENCE: 2
204  Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly
205      1          5          10          15
206  Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
207      20          25          30
208  Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
209      35          40          45
210  Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
211      50          55          60
212  Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
213      65          70          75          80
214  Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
215      85          90          95
216  Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
217      100         105         110
218  Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
219      115         120         125
220  Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
221      130         135         140
222  Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
223      145         150         155         160
224  Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
225      165         170         175
226  Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
227      180         185         190
228  Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
229      195         200         205
230  Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
231      210         215         220
232  Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
233      225         230         235         240
234  Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
235      245         250         255
236  Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
237      260         265         270
238  Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
239      275         280         285
240  Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
241      290         295         300
242  Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
243      305         310         315         320
244  Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
245      325         330         335

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```

246 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
247           340           345           350
248 Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
249           355           360           365
250 Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
251           370           375           380
252 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met
253           385           390           395           400
254 Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
255           405           410           415
256 Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
257           420           425           430
258 Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
259           435           440           445
260 Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
261           450           455           460
262 Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
263           465           470           475           480
264 Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
265           485           490           495
266 Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
267           500           505           510
268 Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
269           515           520           525
270 Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
271           530           535           540
272 Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
273           545           550           555           560
274 Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
275           565           570           575
276 Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
277           580           585           590
278 Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
279           595           600           605
280 Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
281           610           615           620
282 Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
283           625           630           635           640
284 Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
285           645           650           655
286 Ser Gly Gln Gln Val
287           660
289 <210> SEQ ID NO: 3
290 <211> LENGTH: 9
291 <212> TYPE: PRT
292 <213> ORGANISM: Homo sapiens
294 <400> SEQUENCE: 3
295 Ser Phe Asp Gln Val Pro Phe Ser Val
296 1 5

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 3,15,18,24,27
Seq#:6; N Pos. 6,15,18,24,27
Seq#:8; N Pos. 3,6,15,18,24,27
Seq#:10; N Pos. 6,15,18,24,27
Seq#:12; N Pos. 3,15,18,24,27
Seq#:14; N Pos. 3,15,18,24,27
Seq#:16; N Pos. 6,15,18,24,27
Seq#:18; N Pos. 6,15,18,24,27